

## Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/539,105
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics _____ Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor <b>after</b> creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line <b>not exceed</b> 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino _____ Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do <b>not</b> use tab codes between numbers; use <b>space characters</b> , instead.	
4 _____ Non-ASCII	The submitted file was <b>not</b> saved in ASCII(DOS) text, as <b>required</b> by the Sequence Rules. <b>Please ensure your subsequent submission is saved in ASCII text.</b>	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. <b>Per Sequence Rules, each n or Xaa can only represent a single residue.</b> Please present the <b>maximum</b> number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 _____ "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>	
7 _____ Skipped Sequences _____ (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for <b>each</b> skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to <b>include</b> the skipped sequences.	
8 _____ Skipped Sequences _____ (NEW RULES)	Sequence(s) _____ missing. If <b>intentional</b> , please insert the following lines for <b>each</b> skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's _____ (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is <b>MANDATORY</b> if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> _____ Response	Per 1.823 of Sequence Rules, the only <b>valid &lt;213&gt; responses are: Unknown, Artificial Sequence, or scientific name (Genus/species).</b> <220>-<223> section is <b>required</b> when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is <b>MANDATORY</b> if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 _____ "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can <b>only</b> represent a single <u>nucleotide</u> ; "Xaa" can <b>only</b> represent a single <u>amino acid</u>	



PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/539,105

DATE: 06/27/2005

TIME: 11:17:05

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06272005\J539105.raw

5 <110> APPLICANT: Garvan Institute of Medical Research  
 9 <120> TITLE OF INVENTION: Methods of treatment of feeding disorders or disorders of glucose uptake  
 10 and for modifying metabolism and identifying therapeutic reagents therefor  
 14 <130> FILE REFERENCE: 502008/MRO  
 C--> 18 <140> CURRENT APPLICATION NUMBER: US/10/539,105  
 C--> 18 <141> CURRENT FILING DATE: 2005-06-15  
 18 <150> PRIOR APPLICATION NUMBER: AU 2002953393  
 20 <151> PRIOR FILING DATE: 2002-12-16  
 24 <150> PRIOR APPLICATION NUMBER: AU 2003906285  
 26 <151> PRIOR FILING DATE: 2003-11-14  
 30 <160> NUMBER OF SEQ ID NOS: 261  
 34 <170> SOFTWARE: PatentIn version 3.1

## ERRORED SEQUENCES

4948 <210> SEQ ID NO: 251  
 4950 <211> LENGTH: 2721  
 4952 <212> TYPE: DNA  
 4954 <213> ORGANISM: c-Cbl Y700F  
 4958 <220> FEATURE:  
 4960 <221> NAME/KEY: CDS  
 4962 <222> LOCATION: (1)..(2718)  
 4964 <223> OTHER INFORMATION:  
 W--> 4968 <400> 251  
 4969 atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc  
 4970 Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Thr Gly  
 4971 1 5 10 15  
 4973 tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc  
 4974 Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala  
 4975 20 25 30  
 4977 ttc cag ccg cac cac cac cac cac cac ctc agc ccc cac ccg ccg  
 4978 Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro  
 4979 35 40 45  
 4981 ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac  
 4982 Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
 4983 50 55 60  
 E--> 4985 aag ctg gtg cggg tgt cag aac cca aag ctg gcg cta aag aat agc  
 W--> 4986 Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
 4987 65 70 75 80  
 E--> 4989 cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt  
 4990 Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
 4991 85 90 95

Does Not Comply  
 Corrected Diskette Needed

(pg. 1-5)

Found 2719  
 Invalid  
 response

<213> response has  
 to be either Artificial,  
 Unknown or Genus/  
 Species.

48 See item  
 96 #10 on  
 error  
 summary  
 sheet.

more over

240 - 238

288 - 286

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/539,105

DATE: 06/27/2005

TIME: 11:17:05

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06272005\J539105.raw

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E--> 4993 act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat
      4994 Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn
      4995                               100                               105                               110
E--> 4997 gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa
      4998 Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln
      4999                               115                               120                               125
E--> 5001 acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat
      5002 Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn
      5003                               130                               135                               140
E--> 5005 tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac
      5006 Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His
      5007 145                               150                               155                               160
E--> 5009 atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga
      5010 Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly
      5011                               165                               170                               175
E--> 5013 gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa
      5014 Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys
      5015                               180                               185                               190
E--> 5017 gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct
      5018 Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala
      5019                               195                               200                               205
E--> 5021 cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg
      5022 Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu
      5023                               210                               215                               220
E--> 5025 aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa
      5026 Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu
      5027 225                               230                               235                               240
E--> 5029 ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg
      5030 Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg
      5031                               245                               250                               255
E--> 5033 aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg
      5034 Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu
      5035                               260                               265                               270
E--> 5037 acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct
      5038 Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro
      5039                               275                               280                               285
E--> 5041 ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct
      5042 Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala
      5043                               290                               295                               300
E--> 5045 att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac
      5046 Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His
      5047 305                               310                               315                               320
E--> 5049 aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc
      5050 Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe
      5051                               325                               330                               335
E--> 5053 tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta
      5054 Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu
      5055                               340                               345                               350
E--> 5057 tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat

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## RAW SEQUENCE LISTING

DATE: 06/27/2005

PATENT APPLICATION: US/10/539,105

TIME: 11:17:05

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06272005\J539105.raw

	5058	Cys	Glu	Pro	Thr	Pro	Gln	Asp	His	Ile	Lys	Val	Thr	Gln	Glu	Gln	Tyr	
	5059			355					360					365				
E-->	5061	gaa	tta	tac	tgt	gag	atg	ggc	tcc	aca	ttc	caa	cta	tgt	aaa	ata	tgt	1152
	5062	Glu	Leu	Tyr	Cys	Glu	Met	Gly	Ser	Thr	Phe	Gln	Leu	Cys	Lys	Ile	Cys	
	5063		370					375					380					
E-->	5065	gct	gaa	aat	gat	aag	gat	gta	aag	att	gag	ccc	tgt	gga	cac	ctc	atg	1200
	5066	Ala	Glu	Asn	Asp	Lys	Asp	Val	Lys	Ile	Glu	Pro	Cys	Gly	His	Leu	Met	
	5067	385					390				395					400		
E-->	5069	tgc	aca	tcc	tgt	ctt	aca	tcc	tgg	cag	gaa	tca	gaa	ggg	cag	ggc	tgt	1248
	5070	Cys	Thr	Ser	Cys	Leu	Thr	Ser	Trp	Gln	Glu	Ser	Glu	Gly	Gln	Gly	Cys	
	5071				405					410					415			
E-->	5073	cct	ttc	tgc	cga	tgt	gaa	att	aaa	ggg	act	gaa	ccc	atc	gtg	gta	gat	1296
	5074	Pro	Phe	Cys	Arg	Cys	Glu	Ile	Lys	Gly	Thr	Glu	Pro	Ile	Val	Val	Asp	
	5075			420						425				430				
E-->	5077	ccg	ttt	gat	cct	aga	ggg	agt	ggc	agc	ctg	ttg	agg	caa	gga	gca	gag	1344
	5078	Pro	Phe	Asp	Pro	Arg	Gly	Ser	Gly	Ser	Leu	Leu	Arg	Gln	Gly	Ala	Glu	
	5079			435				440					445					
E-->	5081	gga	gct	ccc	tcc	cca	aat	tat	gat	gat	gat	gat	gat	gaa	cga	gct	gat	1392
	5082	Gly	Ala	Pro	Ser	Pro	Asn	Tyr	Asp	Asp	Asp	Asp	Asp	Glu	Arg	Ala	Asp	
	5083		450				455					460						
E-->	5085	gat	act	ctc	ttc	atg	atg	aag	gaa	ttg	gct	ggg	gcc	aag	gtg	gaa	cgg	1440
	5086	Asp	Thr	Leu	Phe	Met	Met	Lys	Glu	Leu	Ala	Gly	Ala	Lys	Val	Glu	Arg	
	5087	465			470					475				480				
E-->	5089	ccg	cct	tct	cca	ttc	tcc	atg	gcc	cca	caa	gct	tcc	ctt	ccc	ccg	gtg	1488
	5090	Pro	Pro	Ser	Pro	Phe	Ser	Met	Ala	Pro	Gln	Ala	Ser	Leu	Pro	Pro	Val	
	5091			485					490				495					
E-->	5093	cca	cca	cga	ctt	gac	ctt	ctg	ccg	cag	cga	gta	tgt	gtt	ccc	tca	agt	1536
	5094	Pro	Pro	Arg	Leu	Asp	Leu	Leu	Pro	Gln	Arg	Val	Cys	Val	Pro	Ser	Ser	
	5095			500					505				510					
E-->	5097	gct	tct	gct	ctt	gga	act	gct	tct	aag	gct	gct	tct	ggc	tcc	ctt	cat	1584
	5098	Ala	Ser	Ala	Leu	Gly	Thr	Ala	Ser	Lys	Ala	Ala	Ser	Gly	Ser	Leu	His	
	5099			515				520					525					
E-->	5101	aaa	gac	aaa	cca	ttg	cca	gta	cct	ccc	aca	ctt	cga	gat	ctt	cca	cca	1632
	5102	Lys	Asp	Lys	Pro	Leu	Pro	Val	Pro	Pro	Thr	Leu	Arg	Asp	Leu	Pro	Pro	
	5103		530				535					540						
E-->	5105	cca	ccg	cct	cca	gac	cgg	cca	tat	tct	gtt	gga	gca	gaa	tcc	cga	cct	1680
	5106	Pro	Pro	Pro	Pro	Asp	Arg	Pro	Tyr	Ser	Val	Gly	Ala	Glu	Ser	Arg	Pro	
	5107	545			550					555				560				
E-->	5109	caa	aga	cgc	ccc	ttg	cct	tgt	aca	cca	ggc	gac	tgt	ccc	tcc	aga	gac	1728
	5110	Gln	Arg	Arg	Pro	Leu	Pro	Cys	Thr	Pro	Gly	Asp	Cys	Pro	Ser	Arg	Asp	
	5111			565					570				575					
E-->	5113	aaa	ctg	ccc	cct	gtc	ccc	tct	agc	cgc	ctt	gga	gac	tca	tgg	ctg	ccc	1776
	5114	Lys	Leu	Pro	Pro	Val	Pro	Ser	Ser	Arg	Leu	Gly	Asp	Ser	Trp	Leu	Pro	
	5115			580				585					590					
E-->	5117	cgg	cca	atc	ccc	aaa	gta	cca	gta	tct	gcc	cca	agt	tcc	agt	gat	ccc	1824
	5118	Arg	Pro	Ile	Pro	Lys	Val	Pro	Val	Ser	Ala	Pro	Ser	Ser	Ser	Asp	Pro	
	5119			595			600						605					
E-->	5121	tgg	aca	gga	aga	gaa	tta	acc	aac	cgg	cac	tca	ctt	cca	ttt	tca	ttg	1872
	5122	Trp	Thr	Gly	Arg	Glu	Leu	Thr	Asn	Arg	His	Ser	Leu	Pro	Phe	Ser	Leu	

Same  
errors

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/539,105

DATE: 06/27/2005

TIME: 11:17:05

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06272005\J539105.raw

5123	610	615	620	
E--> 5125	ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg	1920		
5126	Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr			
5127	625 630 635 640			
E--> 5129	ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt	1968		
5130	Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly			
5131	645 650 655			
E--> 5133	cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc	2016		
5134	Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala			
5135	660 665 670			
E--> 5137	att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct	2064		
5138	Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro			
5139	675 680 685			
E--> 5141	ggg gag caa tgt gag ggt gaa gag gac aca gag ttc atg act ccc tct	2112		
5142	Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Phe Met Thr Pro Ser			
5143	690 695 700			
E--> 5145	tcc agg cct cta cgg cct ttg gat aca tcc cag agt tca cga gca tgt	2160		
5146	Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys			
5147	705 710 715 720			
E--> 5149	gat tgc gac cag cag att gat agc tgt acg tat gaa gca atg tat aat	2208		
5150	Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn			
5151	725 730 735			
E--> 5153	att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa	2256		
5154	Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu			
5155	740 745 750			
E--> 5157	ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa	2304		
5158	Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu			
5159	755 760 765			
E--> 5161	aat gag gat gat ggg tat gat gtc cca aag cca cct gtg ccg gcc gtg	2352		
5162	Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val			
5163	770 775 780			
E--> 5165	ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt	2400		
5166	Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe			
5167	785 790 795 800			
E--> 5169	ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt	2448		
5170	Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly			
5171	805 810 815			
E--> 5173	tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg cgg aga atc aac	2496		
5174	Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn			
5175	820 825 830			
E--> 5177	tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc	2544		
5178	Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala			
5179	835 840 845			
E--> 5181	tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc	2592		
5182	Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu			
5183	850 855 860			
E--> 5185	atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att	2640		
5186	Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile			
5187	865 870 875 880			

Same  
errors

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TIME: 11:17:05

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06272005\J539105.raw

E--> 5189 gcc cag aac aac atc gag atg gcc aaa aac atc ctc cgg gaa ttt gtt 2688  
5190 Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
5191 885 890 895  
E--> 5193 tcc att tct tct cct gcc cat gta gct acc tag 2721  
5194 Ser Ile Ser Ser Pro Ala His Val Ala Thr  
E--> 5195 900 905

2721

2719

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

10/539,105-

Page 6

<210> 4

<211> 21

<212> DNA

<213> siRNA sense strand oligonucleotide

<400> 4

cgtgaagaag agctctgggt t

p/s see item #10  
on error summary  
Sheet

Invalid  
Response

21

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/539,105

DATE: 06/27/2005  
TIME: 11:17:06

Input Set : A:\PTO.RJ.txt  
Output Set: N:\CRF4\06272005\J539105.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 9



## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/539,105

DATE: 06/27/2005

TIME: 11:17:06

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06272005\J539105.raw

L:18 M:270 C: Current Application Number differs, Replaced Current Application No  
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:3988 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:247,Line#:3984  
L:4478 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:249,Line#:4474  
L:4968 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:251,Line#:4964  
L:4985 M:254 E: No. of Bases conflict, LENGTH:Input:240 Counted:238 SEQ:251 ✓  
L:4986 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 251, CDS  
LOCATION:1..2718  
M:254 Repeated in SeqNo=251  
L:5195 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2721 Found:2719 SEQ:251 ✓  
L:5458 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:253,Line#:5454  
L:5948 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:255,Line#:5944  
L:6438 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:257,Line#:6434  
L:6928 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:259,Line#:6924